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LIST OF SEQUENCES

(1) GENERAL INFORMATION:

(i) DEPOSITOR:

(A) NAME: CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
(B) STREET: 3, rue Michel-Ange
(C) CITY: PARIS
(E) COUNTRY: FRANCE
(F) POSTAL CODE: 75794 CEDEX 16

(ii) TITLE OF THE INVENTION: NF- κ B ACTIVATION INHIBITORS, AND
THEIR PHARMACEUTICAL USES

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

(A) TYPE OF SUPPORT: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) USER SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (OEB)

(2) INFORMATION FOR THE SEQ ID NO: 1:

(i) CHARACTERISTICS OF THE SEQUENCE:

(A) LENGTH: 609 base pairs
(B) TYPE: nucleotide
(C) NUMBER OF STRANDS: double
(D) CONFIGURATION: linear

(ii) TYPE OF MOLECULE: ADN (g enomic)

(ix) CHARACTERISTIC:

(A) NAME/KEY: CDS
(B) EMPLACEMENT: 1..609

(xi) DESCRIPTION OF THE SEQUENCE: SEQ ID NO: 1:

ATG GCT ACA GGC TCC CGG ACG TCC CTG CTC CTG GCT TTT GGC CTG CTC 48
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC TTC CCA ACC ATT CCC TTA 96
Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
20 25 30

TCC AGG CTT TTT GAC AAC GCT AGT CTC CGC GCC CAT CGT CTG CAC CAG 144
Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg Leu His Gln
35 40 45

	CTG	GCC	TTT	GAC	ACC	TAC	CAG	GAG	TTT	AAC	CCC	CAG	ACC	TCC	CTC	TGT	192
	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe	Asn	Pro	Gln	Thr	Ser	Leu	Cys	
	50						55					60					
5	TTC	TCA	GAG	TCT	ATT	CCG	ACA	CCC	TCC	AAC	AGG	GAG	GAA	ACA	CAA	CAG	240
	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr	Gln	Gln	
	65					70				75						80	
10	AAA	TCC	AAC	CTA	GAG	CTG	CTC	CGC	ATC	TCC	CTG	CTG	CTC	ATC	CAG	TCG	288
	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile	Gln	Ser	
					85					90					95		
15	TGG	CTG	GAG	CCC	GTG	CAG	TTC	CTC	AGG	AGT	GTC	TTC	GCC	AAC	AGC	CTG	336
	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn	Ser	Leu	
				100					105					110			
20	GTG	TAC	GGC	GCC	TCT	GAC	AGC	AAC	GTC	TAT	GAC	CTC	CTA	AAG	GAC	CTA	384
	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys	Asp	Leu	
			115					120					125				
25	GAG	GAA	GGC	ATC	CAA	ACG	CTG	ATG	GGG	AGG	CTG	GAA	GAT	GGC	AGC	CCC	432
	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	Asp	Gly	Ser	Pro	
		130					135				140						
30	CGG	ACT	GGG	CAG	ATC	TTC	AAG	CAG	ACC	TAC	AGC	AAG	TTC	GAC	ACA	AAC	480
	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp	Thr	Asn	
	145					150					155					160	
35	TCA	CAC	AAC	GAT	GAC	GCA	CTA	CTC	AAG	AAC	TAC	GGG	CTG	CTC	TAC	TGC	528
	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu	Tyr	Cys	
					165					170					175		
40	TTC	AGG	AAG	GAC	ATG	GAC	AAG	GTC	GAG	ACA	TTC	CTG	CGC	ATC	GTG	CAG	576
	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	Arg	Ile	Val	Gln	
				180					185					190			
45	TGC	CGC	TCT	GTG	GAG	GGC	AGC	TGT	GGC	TTC	TAG						609
	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe	*						
			195					200									

(2) INFORMATION FOR THE SEQ ID NO: 2:

45 (i) CHARACTERISTICS OF THE SEQUENCE:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(D) CONFIGURATION: linear

50 (ii) MOLECULE TYPE: protein

(xi) DESCRIPTION OF THE SEQUENCE: SEQ ID NO: 2:

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
 1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
 20 25 30
 5 Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg Leu His Gln
 35 40 45
 Leu Ala Phe Asp Thr Tyr Gln Glu Phe Asn Pro Gln Thr Ser Leu Cys
 50 55 60
 10 Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln
 65 70 75 80
 Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser
 85 90 95
 Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu
 100 105 110
 20 Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu
 115 120 125
 Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro
 130 135 140
 25 Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn
 145 150 155 160
 Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys
 165 170 175
 30 Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln
 180 185 190
 35 Cys Arg Ser Val Glu Gly Ser Cys Gly Phe *
 195 200

(2) INFORMATION FOR THE SEQ ID NO: 3:

40 (i) CHARACTERISTICS OF THE SEQUENCE:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleotide
- (C) NUMBER OF STRANDS: double
- (D) CONFIGURATION: linear

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(ii) MOLECULE TYPE: ADN (genomic)

(ix) CHARACTERISTIC:

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- (A) NAME/KEY: CDS
- (B) EMBLACEMENT: 1..582

(xi) DESCRIPTION OF THE SEQUENCE: SEQ ID NO: 3:

	ATG GGG GTG CAC GAA TGT CCT GCC TGG CTG TGG CTT CTC CTG TCC CTG	48
	Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu	
	205 210 215	
5	CTG TCG CTC CCT CTG GGC CTC CCA GTC CTG GGC GCC CCA CCA CGC CTC	96
	Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu	
	220 225 230 235	
10	ATC TGT GAC AGC CGA GTC CTG GAG AGG TAC CTC TTG GAG GCC AAG GAG	144
	Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu	
	240 245 250	
15	GCC GAG AAT ATC ACG ACG GGC TGT GCT GAA CAC TGC AGC TTG AAT GAG	192
	Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu	
	255 260 265	
20	AAT ATC ACT GTC CCA GAC ACC AAA GTT AAT TTC TAT GCC TGG AAG AGG	240
	Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg	
	270 275 280	
25	ATG GAG GTC GGG CAG CAG GCC GTA GAA GTC TGG CAG GGC CTG GCC CTG	288
	Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu	
	285 290 295	
30	CTG TCG GAA GCT GTC CTG CGG GGC CAG GCC CTG TTG GTC AAC TCT TCC	336
	Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser	
	300 305 310 315	
35	CAG CCG TGG GAG CCC CTG CAG CTG CAT GTG GAT AAA GCC GTC AGT GGC	384
	Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly	
	320 325 330	
40	CTT CGC AGC CTC ACC ACT CTG CTT CGG GCT CTG GGA GCC CAG AAG GAA	432
	Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu	
	335 340 345	
45	GCC ATC TCC CCT CCA GAT GCG GCC TCA GCT GCT CCA CTC CGA ACA ATC	480
	Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile	
	350 355 360	
50	ACT GCT GAC ACT TTC CGC AAA CTC TTC CGA GTC TAC TCC AAT TTC CTC	528
	Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu	
	365 370 375	
55	CGG GGA AAG CTG AAG CTG TAC ACA GGG GAG GCC TGC AGG ACA GGG GAC	576
	Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp	
	380 385 390 395	
60	AGA TGA	582
	Arg *	

(2) INFORMATION FOR THE SEQ ID NO: 4:

(i) CHARACTERISTICS OF THE SEQUENCE:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(D) CONFIGURATION: linear

(ii) TYPE OF MOLECULE: protein

(xi) DESCRIPTION OF THE SEQUENCE: SEQ ID NO: 4:

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu
 1 5 10 15
 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30
 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 35 40 45
 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60
 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80
 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 85 90 95
 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110
 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125
 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 130 135 140
 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160
 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175
 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190
 Arg *